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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/051,186

DATE: 03/26/2002

TIME: 09:31:38

Input Set : N:\Crf3\RULE60\10051186.raw

Output Set: N:\CRF3\03262002\J051186.raw

1 <110> APPLICANT: Adamou, J., et al.
 2 <120> TITLE OF INVENTION: Calcitonin Gene Related Peptide Receptor
 3 <130> FILE REFERENCE: PF129C1
 4 <140> CURRENT APPLICATION NUMBER: 10/051,186
 5 <141> CURRENT FILING DATE: 2002-01-22
 7 <150> PRIOR APPLICATION NUMBER: 09/455,442
 8 <151> PRIOR FILING DATE: 1999-12-06
 11 <150> PRIOR APPLICATION NUMBER: 08/461,250
 12 <151> PRIOR FILING DATE: 1995-06-05
 13 <150> PRIOR APPLICATION NUMBER: PCT/US95/01587
 14 <151> PRIOR FILING DATE: 1995-02-03
 15 <150> PRIOR APPLICATION NUMBER: PCT/US94/09235
 16 <151> PRIOR FILING DATE: 1994-08-16

ENTERED

17 <160> NUMBER OF SEQ ID NOS: 9
 18 <170> SOFTWARE: PatentIn version 3.0
 20 <210> SEQ ID NO: 1

21 <211> LENGTH: 3034

22 <212> TYPE: DNA

23 <213> ORGANISM: Homo sapiens

24 <400> SEQUENCE: 1

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27	tcccaccttg	cttgtgggta	aatctcttct	gcggaatctc	agaaagtaaa	gttccatcct	180
28	gagaatattt	cacaaagaat	ttccttaaga	gctggactgg	gtcttgaccc	ctggaattta	240
29	agaaattctt	aaagacaatg	tcaaatatga	tccaagagaa	aatgtgattt	gagtctggag	300
30	acaattgtgc	atatcgtcta	ataataaaaa	cccatactag	cctatagaaa	acaatatttg	360
31	aataataaaa	accatacta	gcctatagaa	aacaatattt	gaaagattgc	taccactaaa	420
32	aagaaaacta	ctacaacttg	acaagactgc	tgcaaacttc	aattgggtcac	cacaacttga	480
33	caaggttgct	ataaaacaag	attgctacaa	cttctagttt	atggtataca	gcatatttca	540
34	tttgggctta	atgatggaga	aaaagtgtac	cctgtatttt	ctggttctct	tgcctttttt	600
35	tatgattctt	gttacagcag	aattagaaga	gagtcctgag	gactcaattc	agttgggagt	660
36	tactagaaat	aaaatcatga	cagctcaata	tgaatgttac	caaaagatta	tgcaagaccc	720
37	cattcaacaa	gcagaaggcg	tttactgcaa	cagaacctgg	gatggatggc	tctgctggaa	780
38	cgatgttgca	gcaggaactg	aatcaatgca	gctctgccct	gattactttc	aggactttga	840
39	tccatcagaa	aaagttacaa	agatctgtga	ccaagatgga	aactggttta	gacatccagc	900
40	aagcaacaga	acatggacaa	attataccca	gtgtaatgtt	aacacccacg	agaaagtga	960
41	gactgcacta	aatttgtttt	acctgaccat	aattggacac	ggattgtcta	ttgcatcact	1020
42	gcttatctcg	cttggcatat	tctttttatt	caagagccta	agttgccaaa	ggattacctt	1080
43	acacaaaaat	ctgttcttct	catttgtttg	taactctgtt	gtaacaatca	ttcacctcac	1140
44	tgcaagtggc	aacaaccagg	ccttagtagc	cacaaatcct	gttagttgca	aagtgtccca	1200
45	gttcattcat	ctttacctga	tgggctgtaa	ttacttttgg	atgctctgtg	aaggcattta	1260
46	cctacacaca	ctcattgtgg	tggccgtgtt	tgcagagaag	caacatttaa	tgtggtatta	1320
47	ttttcttggc	tggggatttc	cactgattcc	tgcttgata	catgccattg	ctagaagctt	1380

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48      atattacaat gacaattgct ggatcagttc tgatacccat ctectctaca ttatccatgg      1440
49      cccaatttgt gctgctttac tggatgaatct ttttttcttg ttaaattattg tacgcgttct      1500
50      catcaccaag ttaaaagtta cacaccaagc ggaatccaat ctgtacatga aagctgtgag      1560
51      agctactctt atcttggtgc cattgcttgg cattgaattt gtgctgattc catggcgacc      1620
52      tgaaggaaag attgcagagg aggtatatga ctacatcatg cacatcctta tgcacttcca      1680
53      gggctctttg gtctctacca ttttctgctt ctttaattga gaggttcaag caattctgag      1740
54      aagaaactgg aatcaatata aaatccaatt tggaaacagc ttttccaact cagaagctct      1800
55      tcgtagtgcg tcttacacag tgtcaacaat cagtgatggc ccagggtata gtcagtactg      1860
56      tcctagttaa cacttaaattg gaaaaagcat ccatgatatt gaaaatgttc tcttaaaacc      1920
57      agaaaattta tataattgaa aatagaagga tgggtgtctc actgtttggg gcttctccta      1980
58      actcaaggac ttggacccat gactctgtag ccagaagact tcaatattaa atgactttgg      2040
59      ggaatgtcat aaagaagagc cttcacatga aattagtagt gtgttgataa gagtgtaaca      2100
60      tccagctcta tgtgggaaaa aagaaatcct ggtttgtaat gtttgtcagt aaatactccc      2160
61      actatgcctg atgtgacgct actaacctga catcaccaag tgtggaattg gagaaaagca      2220
62      caatcaactt ttctgagctg gtgtaagcca gttccagcac accattgatg aattcaaaca      2280
63      aatggctgta aaactaaaca tacatgttgg gcatgattct acccttattc sccccaagag      2340
64      acctagctaa ggtctataaa catgaaggga aaattagctt ttagttttaa aactctttat      2400
65      cccatcttga ttggggcagt tgactttttt tttttcccag agtgccgtag tcctttttgt      2460
66      aactaccctc tcaaatggac aataccagaa gtgaattatc cctgctggct ttcttttctc      2520
67      tatgaaaagc aactgagtac aattgttatg atctactcat ttgctgacac atcagttata      2580
68      tcttgtggca tatccattgt ggaaactgga tgaacaggat gtataatatg caatcttact      2640
69      tctatatcat taggaaaaca tcttagttga tgctacaaaa caccttgtea acctcttcct      2700
70      gtcttaccaa acagtgggag ggaattccta gctgtaaata taaattttgc ccttccattt      2760
71      ctactgtata aacaaattag caatcatttt atataaagaa aatcaatgaa ggatttctta      2820
72      ttttcttgga attttgtaaa aagaaattgt gaaaaatgag cttgtaaata ctccattatt      2880
73      ttattttata gtctcaaata aaatacatat aacctatgta atttttaag caaatatata      2940
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77 <210> SEQ ID NO: 2

78 <211> LENGTH: 461

79 <212> TYPE: PRT

80 <213> ORGANISM: Homo sapiens

81 <400> SEQUENCE: 2

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84      Met Ile Leu Val Thr Ala Glu Leu Glu Glu Ser Pro Glu Asp Ser Ile
85      20          25          30
86      Gln Leu Gly Val Thr Arg Asn Lys Ile Met Thr Ala Gln Tyr Glu Cys
87      35          40          45
88      Tyr Gln Lys Ile Met Gln Asp Pro Ile Gln Gln Ala Glu Gly Val Tyr
89      50          55          60
90      Cys Asn Arg Thr Trp Asp Gly Trp Leu Cys Trp Asn Asp Val Ala Ala
91      65          70          75          80
92      Gly Thr Glu Ser Met Gln Leu Cys Pro Asp Tyr Phe Gln Asp Phe Asp
93      85          90          95
94      Pro Ser Glu Lys Val Thr Lys Ile Cys Asp Gln Asp Gly Asn Trp Phe
95      100         105         110
96      Arg His Pro Ala Ser Asn Arg Thr Trp Thr Asn Tyr Thr Gln Cys Asn
97      115         120         125

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98 Val Asn Thr His Glu Lys Val Lys Thr Ala Leu Asn Leu Phe Tyr Leu
99      130      135      140
100 Thr Ile Ile Gly His Gly Leu Ser Ile Ala Ser Leu Leu Ile Ser Leu
101      145      150      155      160
102 Gly Ile Phe Phe Tyr Phe Lys Ser Leu Ser Cys Gln Arg Ile Thr Leu
103      165      170      175
104 His Lys Asn Leu Phe Phe Ser Phe Val Cys Asn Ser Val Val Thr Ile
105      180      185      190
106 Ile His Leu Thr Ala Val Ala Asn Asn Gln Ala Leu Val Ala Thr Asn
107      195      200      205
108 Pro Val Ser Cys Lys Val Ser Gln Phe Ile His Leu Tyr Leu Met Gly
109      210      215      220
110 Cys Asn Tyr Phe Trp Met Leu Cys Glu Gly Ile Tyr Leu His Thr Leu
111      225      230      235      240
112 Ile Val Val Ala Val Phe Ala Glu Lys Gln His Leu Met Trp Tyr Tyr
113      245      250      255
114 Phe Leu Gly Trp Gly Phe Pro Leu Ile Pro Ala Cys Ile His Ala Ile
115      260      265      270
116 Ala Arg Ser Leu Tyr Tyr Asn Asp Asn Cys Trp Ile Ser Ser Asp Thr
117      275      280      285
118 His Leu Leu Tyr Ile Ile His Gly Pro Ile Cys Ala Ala Leu Leu Val
119      290      295      300
120 Asn Leu Phe Phe Leu Leu Asn Ile Val Arg Val Leu Ile Thr Lys Leu
121      305      310      315      320
122 Lys Val Thr His Gln Ala Glu Ser Asn Leu Tyr Met Lys Ala Val Arg
123      325      330      335
124 Ala Thr Leu Ile Leu Val Pro Leu Leu Gly Ile Glu Phe Val Leu Ile
125      340      345      350
126 Pro Trp Arg Pro Glu Gly Lys Ile Ala Glu Glu Val Tyr Asp Tyr Ile
127      355      360      365
128 Met His Ile Leu Met His Phe Gln Gly Leu Leu Val Ser Thr Ile Phe
129      370      375      380
130 Cys Phe Phe Asn Gly Glu Val Gln Ala Ile Leu Arg Arg Asn Trp Asn
131      385      390      395      400
132 Gln Tyr Lys Ile Gln Phe Gly Asn Ser Phe Ser Asn Ser Glu Ala Leu
133      405      410      415
134 Arg Ser Ala Ser Tyr Thr Val Ser Thr Ile Ser Asp Gly Pro Gly Tyr
135      420      425      430
136 Ser His Asp Cys Pro Ser Glu His Leu Asn Gly Lys Ser Ile His Asp
137      435      440      445
138 Ile Glu Asn Val Leu Leu Lys Pro Glu Asn Leu Tyr Asn
139      450      455      460
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142 <211> LENGTH: 30
143 <212> TYPE: DNA
144 <213> ORGANISM: Oligonucleotide
145 <400> SEQUENCE: 3
146      gactaaagct taatgttata cagcatatatt
148 <210> SEQ ID NO: 4

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150 <212> TYPE: DNA
151 <213> ORGANISM: Oligonucleotide
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155 <210> SEQ ID NO: 5
156 <211> LENGTH: 34
157 <212> TYPE: DNA
158 <213> ORGANISM: Oligonucleotide
159 <400> SEQUENCE: 5
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163 <211> LENGTH: 34
164 <212> TYPE: DNA
165 <213> ORGANISM: Oligonucleotide
166 <400> SEQUENCE: 6
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169 <210> SEQ ID NO: 7
170 <211> LENGTH: 11
171 <212> TYPE: PRT
172 <213> ORGANISM: Peptide
173 <400> SEQUENCE: 7
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178 <211> LENGTH: 490
179 <212> TYPE: PRT
180 <213> ORGANISM: Homo sapiens
181 <400> SEQUENCE: 8
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184      Asn His Pro Thr Pro Ile Leu Pro Ala Phe Ser Asn Gln Thr Tyr Pro
185      20          25          30
186      Thr Ile Glu Pro Lys Pro Phe Leu Tyr Val Val Gly Arg Lys Lys Met
187      35          40          45
188      Met Asp Ala Gln Tyr Lys Cys Tyr Asp Arg Met Gln Gln Leu Pro Ala
189      50          55          60
190      Tyr Gln Gly Glu Gly Pro Tyr Cys Asn Arg Thr Trp Asp Gly Trp Leu
191      65          70          75          80
192      Cys Trp Asp Asp Thr Pro Ala Gly Val Leu Ser Tyr Gln Phe Cys Pro
193      85          90          95
194      Asp Tyr Phe Pro Asp Phe Asp Pro Ser Glu Lys Val Thr Lys Tyr Cys
195      100          105          110
196      Asp Glu Lys Gly Val Trp Phe Lys His Pro Glu Asn Asn Arg Thr Trp
197      115          120          125
198      Ser Asn Tyr Thr Met Cys Asn Ala Phe Thr Pro Glu Lys Leu Lys Asn
199      130          135          140
200      Ala Tyr Val Leu Tyr Tyr Leu Ala Ile Val Gly His Ser Leu Ser Ile
201      145          150          155          160

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202   Phe Thr Leu Val Ile Ser Leu Gly Ile Phe Val Phe Phe Arg Lys Leu
203               165               170               175
204   Thr Thr Ile Phe Pro Leu Asn Trp Lys Tyr Arg Lys Ala Leu Ser Leu
205               180               185               190
206   Gly Cys Gln Arg Val Thr Leu His Lys Asn Met Phe Leu Thr Tyr Ile
207               195               200               205
208   Leu Asn Ser Met Ile Ile Ile Ile His Leu Val Glu Val Val Pro Asn
209               210               215               220
210   Gly Glu Leu Val Arg Arg Asp Pro Val Ser Cys Lys Ile Leu His Phe
211   225               230               235               240
212   Phe His Gln Tyr Met Met Ala Cys Asn Tyr Phe Trp Met Leu Cys Glu
213               245               250               255
214   Gly Ile Tyr Leu His Thr Leu Ile Val Val Ala Val Phe Thr Glu Lys
215               260               265               270
216   Gln Arg Leu Arg Trp Tyr Tyr Leu Leu Gly Trp Gly Phe Pro Leu Val
217   275               280               285
218   Pro Thr Thr Ile His Ala Ile Thr Arg Ala Val Tyr Phe Asn Asp Asn
219   290               295               300
220   Cys Trp Leu Ser Val Glu Thr His Leu Leu Tyr Ile Ile His Gly Pro
221   305               310               315               320
222   Val Met Ala Ala Leu Val Val Asn Phe Phe Phe Leu Leu Asn Ile Val
223               325               330               335
224   Arg Val Leu Val Thr Lys Met Arg Glu Thr His Glu Ala Glu Ser His
225   340               345               350
226   Met Tyr Leu Lys Ala Val Lys Ala Thr Met Ile Leu Val Pro Leu Leu
227   355               360               365
228   Gly Ile Gln Phe Val Val Phe Pro Trp Arg Pro Ser Asn Lys Met Leu
229   370               375               380
230   Gly Lys Ile Tyr Asp Tyr Val Met His Ser Leu Ile His Phe Gln Gly
231   385               390               395               400
232   Phe Phe Val Ala Thr Ile Tyr Cys Phe Cys Asn Asn Glu Val Gln Thr
233   405               410               415
234   Thr Val Lys Arg Gln Trp Ala Gln Phe Lys Ile Gln Trp Asn Gln Arg
235   420               425               430
236   Trp Gly Arg Arg Pro Ser Asn Arg Ser Ala Arg Ala Ala Ala Ala
237   435               440               445
238   Ala Glu Ala Gly Asp Ile Pro Ile Tyr Ile Cys His Gln Glu Pro Arg
239   450               455               460
240   Asn Glu Pro Ala Asn Asn Gln Gly Glu Glu Ser Ala Glu Ile Ile Pro
241   465               470               475               480
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243   485               490
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246 <211> LENGTH: 464
247 <212> TYPE: PRT
248 <213> ORGANISM: Rat
249 <400> SEQUENCE: 9
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251   1               5               10               15

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VERIFICATION SUMMARY

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